

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Alnemri, Emad S.  
Fernandes-Alnemri, Teresa  
Litwack, Gerald  
Armstrong, Robert  
Tomaselli, Kevin
- (ii) TITLE OF INVENTION: MCH4 AND MCH5, APOPTOTIC PROTEASE,  
NUCLEIC ACIDS ENCODING AND METHODS OF USE
- (iii) NUMBER OF SEQUENCES: 75
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Seed Intellectual Property Law Group
  - (B) STREET: Suite 6300, 701 Fifth Avenue
  - (C) CITY: Seattle
  - (D) STATE: Washington
  - (E) COUNTRY: USA
  - (F) ZIP: 98104
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US
  - (B) FILING DATE: 22-SEPT-2003
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Laherty, Carol D.
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  - (C) REFERENCE/DOCKET NUMBER: 480140.424D1
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1700 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ix) FEATURE:
  - (A) NAME/KEY: CDS

(B) LOCATION: 148..1584

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..1700
- (D) OTHER INFORMATION: /note= "Mch4"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGAAAGTCTCT	TCCCAAGCAA	ATGGGAGCTT	CTTTGGACCT	TGGAGCACAC	AGAGGATTCT	60
ACTTTCTTTA	AAACTTTGTT	TTCAGGCAAT	TTCCCTGAGA	ACCGTTACT	TCCAGAAGAT	120
TGGTGGAGCT	TGATCTGAAG	GCTGGCC	ATG AAA TCT CAA GGT CAA CAT TGG			171
			Met Lys Ser Gln Gly Gln His Trp			
			1	5		
TAT TCC AGT TCA GAT AAA AAC TGT AAA GTG AGC TTT CGT GAG AAG CTT						219
Tyr Ser Ser Ser Asp Lys Asn Cys Lys Val Ser Phe Arg Glu Lys Leu						
10	15	20				
CTG ATT ATT GAT TCA AAC CTG GGG GTC CAA GAT GTG GAG AAC CTC AAG						267
Leu Ile Ile Asp Ser Asn Leu Gly Val Gln Asp Val Glu Asn Leu Lys						
25	30	35	40			
TTT CTC TGC ATA GGA TTG GTC CCC AAC AAG AAG CTG GAG AAG TCC AGC						315
Phe Leu Cys Ile Gly Leu Val Pro Asn Lys Lys Leu Glu Lys Ser Ser						
45	50	55				
TCA GCC TCA GAT GTT TTT GAA CAT CTC TTG GCA GAG GAT CTG CTG AGT						363
Ser Ala Ser Asp Val Phe Glu His Leu Leu Ala Glu Asp Leu Leu Ser						
60	65	70				
GAG GAA GAC CCT TTC CTG GCA GAA CTC CTC TAT ATC ATA CGG CAG						411
Glu Glu Asp Pro Phe Phe Leu Ala Glu Leu Leu Tyr Ile Arg Gln						
75	80	85				
AAG AAG CTG CTG CAG CAC CTC AAC TGT ACC AAA GAG GAA GTG GAG CGA						459
Lys Lys Leu Leu Gln His Leu Asn Cys Thr Lys Glu Glu Val Glu Arg						
90	95	100				
CTG CTG CCC ACC CGA CAA AGG GTT TCT CTG TTT AGA AAC CTG CTC TAC						507
Leu Leu Pro Thr Arg Gln Arg Val Ser Leu Phe Arg Asn Leu Leu Tyr						
105	110	115	120			
GAA CTG TCA GAA GGC ATT GAC TCA GAG AAC TTA AAG GAC ATG ATC TTC						555
Glu Leu Ser Glu Gly Ile Asp Ser Glu Asn Leu Lys Asp Met Ile Phe						
125	130	135				
CTT CTG AAA GAC TCG CTT CCC AAA ACT GAA ATG ACC TCC CTA AGT TTC						603
Leu Leu Lys Asp Ser Leu Pro Lys Thr Glu Met Thr Ser Leu Ser Phe						
140	145	150				
CTG GCA TTT CTA GAG AAA CAA GGT AAA ATA GAT GAA GAT AAT CTG ACA						651
Leu Ala Phe Leu Glu Lys Gln Gly Lys Ile Asp Glu Asp Asn Leu Thr						
155	160	165				

TGC CTG GAG GAC CTC TGC AAA ACA GTT GTA CCT AAA CTT TTG AGA AAC	699
Cys Leu Glu Asp Leu Cys Lys Thr Val Val Pro Lys Leu Leu Arg Asn	
170 175 180	
ATA GAG AAA TAC AAA AGA GAG AAA GCT ATC CAG ATA GTG ACA CCT CCT	747
Ile Glu Lys Tyr Lys Arg Glu Lys Ala Ile Gln Ile Val Thr Pro Pro	
185 190 195 200	
GTA GAC AAG GAA GCC GAG TCG TAT CAA GGA GAG GAA GAA CTA CTT TCC	795
Val Asp Lys Glu Ala Glu Ser Tyr Gln Gly Glu Glu Glu Leu Val Ser	
205 210 215	
CAA ACA GAT GTT AAG ACA TTC TTG GAA GCC TTA CCG AGG GCA GCT GTG	843
Gln Thr Asp Val Lys Thr Phe Leu Glu Ala Leu Pro Arg Ala Ala Val	
220 225 230	
TAC AGG ATG AAT CGG AAC CAC AGA GGC CTC TGT GTC ATT GTC AAC AAC	891
Tyr Arg Met Asn Arg Asn His Arg Gly Leu Cys Val Ile Val Asn Asn	
235 240 245	
CAC AGC TTT ACC TCC CTG AAG GAC AGA CAA GGA ACC CAT AAA GAT GCT	939
His Ser Phe Thr Ser Leu Lys Asp Arg Gln Gly Thr His Lys Asp Ala	
250 255 260	
GAG ATC CTG AGT CAT GTG TTC CAG TGG CTT GGG TTC ACA GTG CAT ATA	987
Glu Ile Leu Ser His Val Phe Gln Trp Leu Gly Phe Thr Val His Ile	
265 270 275 280	
CAC AAT AAT GTG ACG AAA GTG GAA ATG GAG ATG GTC CTG CAG AAG CAG	1035
His Asn Asn Val Thr Lys Val Glu Met Glu Met Val Leu Gln Lys Gln	
285 290 295	
AAG TGC AAT CCA GCC CAT GCC GAC GGG GAC TGC TTC GTG TTC TGT ATT	1083
Lys Cys Asn Pro Ala His Ala Asp Gly Asp Cys Phe Val Phe Cys Ile	
300 305 310	
CTG ACC CAT GGG AGA TTT GGA GCT GTC TAC TCT TCG GAT GAG GCC CTC	1131
Leu Thr His Gly Arg Phe Gly Ala Val Tyr Ser Ser Asp Glu Ala Leu	
315 320 325	
ATT CCC ATT CGG GAG ATC ATG TCT CAC TTC ACA GCC CTG CAG TGC CCT	1179
Ile Pro Ile Arg Glu Ile Met Ser His Phe Thr Ala Leu Gln Cys Pro	
330 335 340	
AGA CTG GCT GAA AAA CCT AAA CTC TTT TTC ATC CAG GCC TGC CAA GGT	1227
Arg Leu Ala Glu Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Gln Gly	
345 350 355 360	
GAA GAG ATA CAG CCT TCC GTA TCC ATC GAA GCA GAT GCT CTG AAC CCT	1275
Glu Glu Ile Gln Pro Ser Val Ser Ile Glu Ala Asp Ala Leu Asn Pro	
365 370 375	
GAG CAG GCA CCC ACT TCC CTG CAG GAC AGT ATT CCT GCC GAG GCT GAC	1323
Glu Gln Ala Pro Thr Ser Leu Gln Asp Ser Ile Pro Ala Glu Ala Asp	
380 385 390	

TTC CTA CTT GGT CTG GCC ACT GTC CCA GGC TAT GTA TCC TTT CGG CAT	1371
Phe Leu Leu Gly Leu Ala Thr Val Pro Gly Tyr Val Ser Phe Arg His	
395 400 405	
GTG GAG GAA GGC AGC TGG TAT ATT CAG TCT CTG TGT AAT CAT CTG AAG	1419
Val Glu Glu Gly Ser Trp Tyr Ile Gln Ser Leu Cys Asn His Leu Lys	
410 415 420	
AAA TTG GTC CCA AGA CAT GAA GAC ATC TTA TCC ATC CTC ACT GCT GTC	1467
Lys Leu Val Pro Arg His Glu Asp Ile Leu Ser Ile Leu Thr Ala Val	
425 430 440	
AAC GAT GAT GTG AGT CGA AGA GTG GAC AAA CAG GGA ACA AAG AAA CAG	1515
Asn Asp Asp Val Ser Arg Arg Val Asp Lys Gln Gly Thr Lys Lys Gln	
445 450 455	
ATG CCC CAG CCT GCT TTC ACA CTA AGG AAA AAA CTA GTA TTC CCT GTG	1563
Met Pro Gln Pro Ala Phe Thr Leu Arg Lys Lys Leu Val Phe Pro Val	
460 465 470	
CCC CTG GAT GCA CTT TCA ATA TAGCAGAGAG TTTTGNTGG TTCTTAGACC	1614
Pro Leu Asp Ala Leu Ser Ile	
475	
TCAAACGAAT CATTGGNTAT AACCTCCAGC CTCCTGCCCA GCACAGGAAT CGGTGGTCTC	1674
CACCTGTCAT TCTAGAAACA GGAAAC	1700

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 479 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Ser Gln Gly Gln His Trp Tyr Ser Ser Ser Asp Lys Asn Cys	
1 5 10 15	
Lys Val Ser Phe Arg Glu Lys Leu Leu Ile Ile Asp Ser Asn Leu Glv	
20 25 30	
Val Gln Asp Val Glu Asn Leu Lys Phe Leu Cys Ile Gly Leu Val Pro	
35 40 45	
Asn Lys Lys Leu Glu Lys Ser Ser Ser Ala Ser Asp Val Phe Glu His	
50 55 60	
Leu Leu Ala Glu Asp Leu Leu Ser Glu Glu Asp Pro Phe Phe Leu Ala	
65 70 75 80	
Glu Leu Leu Tyr Ile Ile Arg Gln Lys Lys Leu Leu Gln His Leu Asn	
85 90 95	

Cys Thr Lys Glu Glu Val Glu Arg Leu Leu Pro Thr Arg Gln Arg Val  
 100 105 110  
 Ser Leu Phe Arg Asn Leu Leu Tyr Glu Leu Ser Glu Gly Ile Asp Ser  
 115 120 125  
 Glu Asn Leu Lys Asp Met Ile Phe Leu Leu Lys Asp Ser Leu Pro Lys  
 130 135 140  
 Thr Glu Met Thr Ser Leu Ser Phe Leu Ala Phe Leu Glu Lys Gln Gly  
 145 150 155 160  
 Lys Ile Asp Glu Asp Asn Leu Thr Cys Leu Glu Asp Leu Cys Lys Thr  
 165 170 175  
 Val Val Pro Lys Leu Leu Arg Asn Ile Glu Lys Tyr Lys Arg Glu Lys  
 180 185 190  
 Ala Ile Gln Ile Val Thr Pro Pro Val Asp Lys Glu Ala Glu Ser Tyr  
 195 200 205  
 Gln Gly Glu Glu Glu Leu Val Ser Gln Thr Asp Val Lys Thr Phe Leu  
 210 215 220  
 Glu Ala Leu Pro Arg Ala Ala Val Tyr Arg Met Asn Arg Asn His Arg  
 225 230 235 240  
 Gly Leu Cys Val Ile Val Asn Asn His Ser Phe Thr Ser Leu Lys Asp  
 245 250 255  
 Arg Gln Gly Thr His Lys Asp Ala Glu Ile Leu Ser His Val Phe Gln  
 260 265 270  
 Trp Leu Gly Phe Thr Val His Ile His Asn Asn Val Thr Lys Val Glu  
 275 280 285  
 Met Glu Met Val Leu Gln Lys Gln Lys Cys Asn Pro Ala His Ala Asp  
 290 295 300  
 Gly Asp Cys Phe Val Phe Cys Ile Leu Thr His Gly Arg Phe Gly Ala  
 305 310 315 320  
 Val Tyr Ser Ser Asp Glu Ala Leu Ile Pro Ile Arg Glu Ile Met Ser  
 325 330 335  
 His Phe Thr Ala Leu Gln Cys Pro Arg Leu Ala Glu Lys Pro Lys Leu  
 340 345 350  
 Phe Phe Ile Gln Ala Cys Gln Gly Glu Glu Ile Gln Pro Ser Val Ser  
 355 360 365  
 Ile Glu Ala Asp Ala Leu Asn Pro Glu Gln Ala Pro Thr Ser Leu Gln  
 370 375 380  
 Asp Ser Ile Pro Ala Glu Ala Asp Phe Leu Leu Gly Leu Ala Thr Val  
 385 390 395 400

Pro Gly Tyr Val Ser Phe Arg His Val Glu Glu Gly Ser Trp Tyr Ile  
 405 410 415  
 Gln Ser Leu Cys Asn His Leu Lys Lys Leu Val Pro Arg His Glu Asp  
 420 425 430  
 Ile Leu Ser Ile Leu Thr Ala Val Asn Asp Asp Val Ser Arg Arg Val  
 435 440 445  
 Asp Lys Gln Gly Thr Lys Lys Gln Met Pro Gln Pro Ala Phe Thr Leu  
 450 455 460  
 Arg Lys Lys Leu Val Phe Pro Val Pro Leu Asp Ala Leu Ser Ile  
 465 470 475

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1883 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 257..1744

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..1883
- (D) OTHER INFORMATION: /note= "Mch5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGAAGGCTGG TTGTTCAGAC TGAGCTTCCT GCCTGCCTGT ACCCCGCCAA CAGCTTCAGA	60
AGAAGGTGAC TGGTGGCTGC CTGAGGAATA CCAGTGGGCA AGAGAATTAG CATTCTGGA	120
GCATCTGCTG TCTGAGCAGC CCCTGGGTGC GTCCACTTTC TGGGCACGTG AGGTTGGGCC	180
TTGGCCGCCT GAGCCCTTGA GTTGGTCACT TGAACCTTGG GAATATTGAG ATTATATTCT	240
CCTGCCTTTT AAAAAG ATG GAC TTC AGC AGA AAT CTT TAT GAT ATT GGG Met Asp Phe Ser Arg Asn Leu Tyr Asp Ile Gly	289
1 5 10	
GAA CAA CTG GAC AGT GAA GAT CTG GCC TCC CTC AAG TTC CTG AGC CTG Glu Gln Leu Asp Ser Glu Asp Leu Ala Ser Leu Lys Phe Leu Ser Leu	337
15 20 25	
GAC TAC ATT CCG CAA AGG AAG CAA GAA CCC ATC AAG GAT GCC TTG ATG Asp Tyr Ile Pro Gln Arg Lys Gln Glu Pro Ile Lys Asp Ala Leu Met	385
30 35 40	

TTA TTC CAG AGA CTC CAG GAA AAG AGA ATG TTG GAG GAA AGC AAT CTG	433
Leu Phe Gln Arg Leu Gln Glu Lys Arg Met Leu Glu Glu Ser Asn Leu	
45 50 55	
TCC TTC CTG AAG GAG CTG CTC CGA ATT AAT AGA CTG GAT TTG CTG	481
Ser Phe Leu Lys Glu Leu Leu Phe Arg Ile Asn Arg Leu Asp Leu Leu	
60 65 70 75	
ATT ACC TAC CTA AAC ACT AGA AAG GAG GAG ATG GAA AGG GAA CTT CAG	529
Ile Thr Tyr Leu Asn Thr Arg Lys Glu Glu Met Glu Arg Glu Leu Gln	
80 85 90	
ACA CCA GGC AGG GCT CAA ATT TCT GCC TAC AGG TTC CAC TTC TGC CGC	577
Thr Pro Gly Arg Ala Gln Ile Ser Ala Tyr Arg Phe His Phe Cys Arg	
95 100 105	
ATG AGC TGG GCT GAA GCA AAC AGC CAG TGC CAG ACA CAG TCT GTA CCT	625
Met Ser Trp Ala Glu Ala Asn Ser Gln Cys Gln Thr Gln Ser Val Pro	
110 115 120	
TTC TGG CGG AGG GTC GAT CAT CTA TTA ATA AGG GTC ATG CTC TAT CAG	673
Phe Trp Arg Arg Val Asp His Leu Leu Ile Arg Val Met Leu Tyr Gln	
125 130 135	
ATT TCA GAA GAA GTG AGC AGA TCA GAA TTG AGG TCT TTT AAG TTT CTT	721
Ile Ser Glu Glu Val Ser Arg Ser Glu Leu Arg Ser Phe Lys Phe Leu	
140 145 150 155	
TTG CAA GAG GAA ATC TCC AAA TGC AAA CTG GAT GAT GAC ATG AAC CTG	769
Leu Gln Glu Glu Ile Ser Lys Cys Lys Leu Asp Asp Asp Met Asn Leu	
160 165 170	
CTG GAT ATT TTC ATA GAG ATG GAG AAG AGG GTC ATC CTG GGA GAA GGA	817
Leu Asp Ile Phe Ile Glu Met Glu Lys Arg Val Ile Leu Gly Glu Gly	
175 180 185	
AAG TTG GAC ATC CTG AAA AGA GTC TGT GCC CAA ATC AAC AAG AGC CTG	865
Lys Leu Asp Ile Leu Lys Arg Val Cys Ala Gln Ile Asn Lys Ser Leu	
190 195 200	
CTG AAG ATA ATC AAC GAC TAT GAA GAA TTC AGC AAA GGG GAG GAG TTG	913
Leu Lys Ile Ile Asn Asp Tyr Glu Glu Phe Ser Lys Gly Glu Glu Leu	
205 210 215	
TGT GGG GTA ATG ACG ATG TCG GAC TGT CCA AGA GAA CAG GAT AGT GAA	961
Cys Gly Val Met Thr Met Ser Asp Cys Pro Arg Glu Gln Asp Ser Glu	
220 225 230 235	
TCA CAG ACT TTG GAC AAA GTT TAC CAA ATG AAA AGC AAG CCT CGG GGA	1009
Ser Gln Thr Leu Asp Lys Val Tyr Gln Met Lys Ser Lys Pro Arg Gly	
240 245 250	
TAC TGT CTG ATC ATC AAC AAT CAC AAT TTT GCA AAA GCA CGG GAG AAA	1057
Tyr Cys Leu Ile Ile Asn Asn His Asn Phe Ala Lys Ala Arg Glu Lys	
255 260 265	

GTG CCC AAA CTT CAC AGC ATT AGG GAC AGG AAT GGA ACA CAC TTG GAT Val Pro Lys Leu His Ser Ile Arg Asp Arg Asn Gly Thr His Leu Asp 270 275 280	1105
GCA GGG GCT TTG ACC ACG ACC TTT GAA GAG CTT CAT TTT GAG ATC AAG Ala Gly Ala Leu Thr Thr Phe Glu Glu Leu His Phe Glu Ile Lys 285 290 295	1153
CCC CAC CAT GAC TGC ACA GTA GAG CAA ATC TAT GAG ATT TTG AAA ATC Pro His His Asp Cys Thr Val Glu Gln Ile Tyr Glu Ile Leu Lys Ile 300 305 310 315	1201
TAC CAA CTC ATG GAC CAC AGT AAC ATG GAC TGC TTC ATC TGC TGT ATC Tyr Gln Leu Met Asp His Ser Asn Met Asp Cys Phe Ile Cys Cys Ile 320 325 330	1249
CTC TCC CAT GGA GAC AAG GGC ATC ATC TAT GGC ACT GAT GGA CAG GAG Leu Ser His Gly Asp Lys Gly Ile Ile Tyr Gly Thr Asp Gly Gln Glu 335 340 345	1297
GCC CCC ATC TAT GAG CTG ACA TCT CAG TTC ACT GGT TTG AAG TGC CCT Ala Pro Ile Tyr Glu Leu Thr Ser Gln Phe Thr Gly Leu Lys Cys Pro 350 355 360	1345
TCC CTT GCT GGA AAA CCC AAA GTG TTT TTT ATT CAG GCT TGT CAG GGG Ser Leu Ala Gly Lys Pro Lys Val Phe Ile Gln Ala Cys Gln Gly 365 370 375	1393
GAT AAC TAC CAG AAA GGT ATA CCT GTT GAG ACT GAT TCA GAG GAG CAA Asp Asn Tyr Gln Lys Gly Ile Pro Val Glu Thr Asp Ser Glu Glu Gln 380 385 390 395	1441
CCC TAT TTA GAA ATG GAT TTA TCA TCA CCT CAA ACG AGA TAT ATC CCG Pro Tyr Leu Glu Met Asp Leu Ser Ser Pro Gln Thr Arg Tyr Ile Pro 400 405 410	1489
GAT GAG GCT GAC TTT CTG CTG GGG ATG GCC ACT GTG AAT AAC TGT GTT Asp Glu Ala Asp Phe Leu Leu Gly Met Ala Thr Val Asn Asn Cys Val 415 420 425	1537
TCC TAC CGA AAC CCT GCA GAG GGA ACC TGG TAC ATC CAG TCA CTT TGC Ser Tyr Arg Asn Pro Ala Glu Gly Thr Trp Tyr Ile Gln Ser Leu Cys 430 435 440	1585
CAG AGC CTG AGA GAG CGA TGT CCT CGA GGC GAT GAT ATT CTC ACC ATC Gln Ser Leu Arg Glu Arg Cys Pro Arg Gly Asp Asp Ile Leu Thr Ile 445 450 455	1633
CTG ACT GAA GTG AAC TAT GAA GTA AGC AAC AAG GAT GAC AAG AAA AAC Leu Thr Glu Val Asn Tyr Glu Val Ser Asn Lys Asp Asp Lys Lys Asn 460 465 470 475	1681
ATG GGG AAA CAG ATG CCT CAG CCT ACT TTC ACA CTA AGA AAA AAA CTT Met Gly Lys Gln Met Pro Gln Pro Thr Phe Thr Leu Arg Lys Lys Leu 480 485 490	1729
GTC TTC CCT TCT GAT TGATGGTGCT ATTTTGTGTTG TTTTGTGTTG TTTTGTGTTT	1784

Val Phe Pro Ser Asp  
495

TTGAGACAGA ATCTCGCTCT GTCGCCAGG CTGGAGTGCA GTGGCGTGAT CTCGGCTCAC 1844  
CGCAAGCTCC GCCTCCCGGG TTCAGGCCAT TCTCCTGCT 1883

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 496 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Phe Ser Arg Asn Leu Tyr Asp Ile Gly Glu Gln Leu Asp Ser  
1 5 10 15

Glu Asp Leu Ala Ser Leu Lys Phe Leu Ser Leu Asp Tyr Ile Pro Gln  
20 25 30

Arg Lys Gln Glu Pro Ile Lys Asp Ala Leu Met Leu Phe Gln Arg Leu  
35 40 45

Gln Glu Lys Arg Met Leu Glu Glu Ser Asn Leu Ser Phe Leu Lys Glu  
50 55 60

Leu Leu Phe Arg Ile Asn Arg Leu Asp Leu Leu Ile Thr Tyr Leu Asn  
65 70 75 80

Thr Arg Lys Glu Glu Met Glu Arg Glu Leu Gln Thr Pro Gly Arg Ala  
85 90 95

Gln Ile Ser Ala Tyr Arg Phe His Phe Cys Arg Met Ser Trp Ala Glu  
100 105 110

Ala Asn Ser Gln Cys Gln Thr Gln Ser Val Pro Phe Trp Arg Arg Val  
115 120 125

Asp His Leu Leu Ile Arg Val Met Leu Tyr Gln Ile Ser Glu Glu Val  
130 135 140

Ser Arg Ser Glu Leu Arg Ser Phe Lys Phe Leu Leu Gln Glu Glu Ile  
145 150 155 160

Ser Lys Cys Lys Leu Asp Asp Asp Met Asn Leu Leu Asp Ile Phe Ile  
165 170 175

Glu Met Glu Lys Arg Val Ile Leu Gly Glu Gly Lys Leu Asp Ile Leu  
180 185 190

Lys Arg Val Cys Ala Gln Ile Asn Lys Ser Leu Leu Lys Ile Ile Asn  
195 200 205

Asp Tyr Glu Glu Phe Ser Lys Gly Glu Glu Leu Cys Gly Val Met Thr  
 210 215 220  
 Met Ser Asp Cys Pro Arg Glu Gln Asp Ser Glu Ser Gln Thr Leu Asp  
 225 230 235 240  
 Lys Val Tyr Gln Met Lys Ser Lys Pro Arg Gly Tyr Cys Leu Ile Ile  
 245 250 255  
 Asn Asn His Asn Phe Ala Lys Ala Arg Glu Lys Val Pro Lys Leu His  
 260 265 270  
 Ser Ile Arg Asp Arg Asn Gly Thr His Leu Asp Ala Gly Ala Leu Thr  
 275 280 285  
 Thr Thr Phe Glu Glu Leu His Phe Glu Ile Lys Pro His His Asp Cys  
 290 295 300  
 Thr Val Glu Gln Ile Tyr Glu Ile Leu Lys Ile Tyr Gln Leu Met Asp  
 305 310 315 320  
 His Ser Asn Met Asp Cys Phe Ile Cys Cys Ile Leu Ser His Gly Asp  
 325 330 335  
 Lys Gly Ile Ile Tyr Gly Thr Asp Gly Gln Glu Ala Pro Ile Tyr Glu  
 340 345 350  
 Leu Thr Ser Gln Phe Thr Gly Leu Lys Cys Pro Ser Leu Ala Gly Lys  
 355 360 365  
 Pro Lys Val Phe Phe Ile Gln Ala Cys Gln Gly Asp Asn Tyr Gln Lys  
 370 375 380  
 Gly Ile Pro Val Glu Thr Asp Ser Glu Glu Gln Pro Tyr Leu Glu Met  
 385 390 395 400  
 Asp Leu Ser Ser Pro Gln Thr Arg Tyr Ile Pro Asp Glu Ala Asp Phe  
 405 410 415  
 Leu Leu Gly Met Ala Thr Val Asn Asn Cys Val Ser Tyr Arg Asn Pro  
 420 425 430  
 Ala Glu Gly Thr Trp Tyr Ile Gln Ser Leu Cys Gln Ser Leu Arg Glu  
 435 440 445  
 Arg Cys Pro Arg Gly Asp Asp Ile Leu Thr Ile Leu Thr Glu Val Asn  
 450 455 460  
 Tyr Glu Val Ser Asn Lys Asp Asp Lys Lys Asn Met Gly Lys Gln Met  
 465 470 475 480  
 Pro Gln Pro Thr Phe Thr Leu Arg Lys Lys Leu Val Phe Pro Ser Asp  
 485 490 495

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..19
- (D) OTHER INFORMATION: /note= "t96-pr1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCAGCCTCGG CAGGAATAC

19

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "SK-Zap"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAGGAATTAG GCACGAG

17

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "Mch5-pr1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACAGAGCGA GATTCTGT

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "Mch5-pr2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCACCATCAA TCAGAAGG

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /note= "Mch5-pr5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGAGATCA TGTCTCAC

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gln Ala Cys Gln Gly

1

5

## (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

1	Gln Ala Cys Arg Gly	5
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## (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "Mch5"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

1	Arg Asp Arg Asn Gly Thr	5
---	-------------------------	---

## (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "Mch5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Leu Ser His Gly Asp Lys  
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..9  
(D) OTHER INFORMATION: /note= "Mch5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Phe Ile Gln Ala Cys Gln Gly Asp Asn  
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..5  
(D) OTHER INFORMATION: /note= "Mch5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Glu Thr Asp Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "Mch5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn	Cys	Val	Ser	Tyr	Arg	Asn	Pro	Ala	Glu	Gly	Thr	Trp	Tyr	Ile
1														15

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "Mch4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys	Asp	Arg	Gln	Gly	Thr
1					5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "Mch4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Leu Thr His Gly Arg Phe

1

5

## (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..9
- (D) OTHER INFORMATION: /note= "Mch4"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Phe Ile Gln Ala Cys Gln Gly Glu Glu  
1 5

## (2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "Mch4"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile Glu Ala Asp Ala  
1 5

## (2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "Mch4"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly Tyr Val Ser Phe Arg His Val Glu Glu Gly Ser Trp Tyr Ile  
1                           5   10   15

## (2) INFORMATION FOR SEQ ID NO:22:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "Mch3"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Val Arg Asn Gly Thr  
1                           5

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "Mch3"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Leu Ser His Gly Glu Glu  
1                           5

## (2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..9
- (D) OTHER INFORMATION: /note= "Mch3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Phe Ile Gln Ala Cys Arg Gly Thr Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "Mch3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Ile Gln Ala Asp Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "Mch3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp Phe Val  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "Mch2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Pro Glu Arg Arg Gly Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "Mch2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Ser His Gly Glu Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: Peptide
  - (B) LOCATION: 1..6
  - (D) OTHER INFORMATION: /note= "Mch2"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ile Ile Gln Ala Cys Arg Gly Asn Gln  
1 5
- (2) INFORMATION FOR SEQ ID NO:30:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 5 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Peptide
    - (B) LOCATION: 1..5
    - (D) OTHER INFORMATION: /note= "Mch2"
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Thr Glu Val Asp Ala  
1 5
  - (2) INFORMATION FOR SEQ ID NO:31:
    - (i) SEQUENCE CHARACTERISTICS:
      - (A) LENGTH: 15 amino acids
      - (B) TYPE: amino acid
      - (C) STRANDEDNESS:
      - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: peptide
    - (ix) FEATURE:
      - (A) NAME/KEY: Peptide
      - (B) LOCATION: 1..15
      - (D) OTHER INFORMATION: /note= "Mch2"
    - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gly Tyr Tyr Ser His Arg Glu Thr Val Asn Gly Ser Trp Tyr Ile  
 1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "CPP32"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Thr Ser Arg Ser Gly Thr  
 1 5

## (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "CPP32"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Leu Ser His Gly Glu Glu  
 1 5

## (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..9  
(D) OTHER INFORMATION: /note= "CPP32"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ile Ile Gln Ala Cys Arg Gly Thr Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..5  
(D) OTHER INFORMATION: /note= "CPP32"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ile Glu Thr Asp Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..15  
(D) OTHER INFORMATION: /note= "CPP32"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Tyr Tyr Ser Trp Arg Asn Ser Lys Asp Gly Ser Trp Phe Ile  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..6  
(D) OTHER INFORMATION: /note= "CED-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Pro Thr Arg Asn Gly Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..6  
(D) OTHER INFORMATION: /note= "CED-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Leu Ser His Gly Glu Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..9

(D) OTHER INFORMATION: /note= "CED-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Phe Val Gln Ala Cys Arg Gly Glu Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..5  
(D) OTHER INFORMATION: /note= "CED-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Asp Ser Val Asp Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..15  
(D) OTHER INFORMATION: /note= "CED-3"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Gln Tyr Val Ser Trp Arg Asn Ser Ala Arg Gly Ser Trp Phe Ile  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "ICE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Pro Arg Arg Thr Gly Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "ICE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Ser His Gly Ile Arg  
1 5

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..9
- (D) OTHER INFORMATION: /note= "ICE"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ile Ile Gln Ala Cys Arg Gly Asp Ser  
 1 5

## (2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..5  
 (D) OTHER INFORMATION: /note= "ICE"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Trp Phe Lys Asp Ser  
 1 5

## (2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..15  
 (D) OTHER INFORMATION: /note= "ICE"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Asp Asn Val Ser Trp Arg His Pro Thr Met Gly Ser Val Phe Ile  
 1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..6  
(D) OTHER INFORMATION: /note= "TX"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Pro Pro Arg Asn Gly Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..6  
(D) OTHER INFORMATION: /note= "TX"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Ser His Gly Ile Leu  
1 5

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..9  
(D) OTHER INFORMATION: /note= "TX"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ile Val Gln Ala Cys Arg Gly Ala Asn  
1 5

## (2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "TX"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Trp	Val	Lys	Asp	Ser	
				5	
1					

## (2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "TX"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

His	Asn	Val	Ser	Trp	Arg	Asp	Ser	Thr	Met	Gly	Ser	Ile	Phe	Ile
								10					15	
1														

## (2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide

(B) LOCATION: 1..6  
 (D) OTHER INFORMATION: /note= "ICEr1III"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Pro Ala Arg Asn Gly Ala  
 1 5

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..6  
 (D) OTHER INFORMATION: /note= "ICEr1III"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Ser His Gly Ile Leu  
 1 5

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 9 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Peptide  
 (B) LOCATION: 1..9  
 (D) OTHER INFORMATION: /note= "ICEr1III"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Ile Val Gln Ala Cys Arg Gly Glu Lys  
 1 5

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "ICERelIII"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Trp	Val	Arg	Asp	Ser
1				5

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "ICERelIII"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

His	Asn	Val	Ser	Trp	Arg	Asp	Arg	Thr	Arg	Gly	Ser	Ile	Phe	Ile
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "ICH-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Glu Phe Arg Ser Gly Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..6  
(D) OTHER INFORMATION: /note= "ICH-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu Ser His Gly Val Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..9  
(D) OTHER INFORMATION: /note= "ICH-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Phe Ile Gln Ala Cys Arg Gly Asp Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "ICH-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Gln Gln Asp Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /note= "ICH-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gly Thr Ala Ala Met Arg Asn Thr Lys Arg Gly Ser Trp Tyr Ile  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CCTACAGGAT CCACTTCTGC CGCATGAGC

29

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACTCCTCCCC TTTGCTGAAT TCTTAATAGT CGT

33

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Peptide  
(B) LOCATION: 1..84  
(D) OTHER INFORMATION: /note= "human FADD"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: .
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..79
- (D) OTHER INFORMATION: /note= "Mch4 A"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Val	Ser	Phe	Arg	Glu	Lys	Leu	Leu	Ile	Ile	Asp	Ser	Asn	Leu	Gly	Val
1				5					10						15
Gln	Asp	Val	Glu	Asn	Leu	Lys	Phe	Leu	Cys	Ile	Gly	Leu	Val	Pro	Asn
							20						30		
Lys	Lys	Leu	Glu	Lys	Ser	Ser	Ala	Ser	Asp	Val	Phe	Glu	His	Leu	
						35						45			
Leu	Ala	Glu	Asp	Leu	Leu	Ser	Glu	Glu	Asp	Pro	Phe	Phe	Leu	Ala	Glu
						50						60			
Leu	Leu	Tyr	Ile	Ile	Arg	Gln	Lys	Lys	Leu	Leu	Gln	His	Leu	Asn	
					70							75			

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: /note= "Mch5 A"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ser	Arg	Asn	Leu	Tyr	Asp	Ile	Gly	Glu	Gln	Leu	Asp	Ser	Glu	Asp	Leu
1					5				10						15
Ala	Ser	Leu	Lys	Phe	Leu	Ser	Leu	Asp	Thr	Ile	Pro	Gln	Arg	Lys	Gln
					20				25				30		
Glu	Pro	Ile	Lys	Asp	Ala	Leu	Met	Leu	Phe	Gln	Arg	Leu	Gln	Glu	Lys
							35						45		
Arg	Met	Leu	Glu	Glu	Ser	Asn	Leu	Ser	Phe	Leu	Lys	Glu	Leu	Leu	Phe
							50						60		
Arg	Ile	Asn	Arg	Leu	Asp	Leu	Leu	Ile	Thr	Tyr					
							65			75					

## (2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..78  
(D) OTHER INFORMATION: /note= "Mch4 B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Val Ser Leu Phe Arg Asn Leu Leu Tyr Glu Leu Ser Glu Gly Ile Asp  
1 5 10 15

Ser Glu Asn Leu Lys Asp Met Ile Phe Leu Leu Lys Asp Ser Leu Pro  
20 25 30

Lys Thr Glu Met Thr Ser Leu Ser Phe Leu Ala Phe Leu Glu Lys Gln  
 35 40 45

Gly Lys Ile Asp Glu Asp Asn Leu Thr Cys Leu Glu Asp Leu Cys Lys  
 50 55 60

Thr Val Val Pro Lys Leu Leu Arg Asn Ile Glu Lys Tyr Lys  
65 70 75

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: Peptide  
(B) LOCATION: 1..79  
(D) OTHER INFORMATION: /note= "Mch5 B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Val Asp His Leu Leu Ile Arg Val Met Leu Tyr Gln Ile Ser Glu Glu  
1 5 10 15

Val Ser Arg Ser Glu Leu Arg Ser Phe Lys Phe Leu Leu Gln Glu Glu  
20 25 30

Ile Ser Lys Cys Lys Leu Asp Asp Asp Met Asn Leu Leu Asp Ile Phe

35	40	45													
Ile	Glu	Met	Glu	Lys	Arg	Val	Ile	Leu	Gly	Glu	Gly	Lys	Leu	Asp	Ile
50						55					60				
Leu	Lys	Arg	Val	Cys	Ala	Gln	Ile	Asn	Lys	Ser	Leu	Leu	Lys	Ile	
65							70						75		

## (2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Gly	Ser
1	5
Trp	Phe
	Ile

## (2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Gly	Ser
1	5
Trp	Tyr
	Ile

## (2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Asp	Glu
Asp	Val
	Asp

1

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Tyr Val Ala Asp  
1

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ile Glu Thr Asp Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ile Gln Ala Asp Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ile Glu Ala Asp Ala  
1 5